

2/22



OIEP

RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/10/034,985

TIME: 10:23:11

Input Set : N:\Crf3\RULE60\10034985.raw.txt

Output Set: N:\CRF3\02282002\J034985.raw

1 <110> APPLICANT: Kretz, Keith
 2 <120> TITLE OF INVENTION: NOVEL PHYTASE
 3 <130> FILE REFERENCE: 09010/029003
 4 <140> CURRENT APPLICATION NUMBER: 10/034,985
 5 <141> CURRENT FILING DATE: 2001-12-21
 6 <150> PRIOR APPLICATION NUMBER: US/09/580,515
 7 <151> PRIOR FILING DATE: 1999-05-25
 8 <150> PRIOR APPLICATION NUMBER: 09/291,931
 9 <151> PRIOR FILING DATE: 1999-04-13
 10 <150> PRIOR APPLICATION NUMBER: 08/910,798
 11 <151> PRIOR FILING DATE: 1997-08-13
 12 <150> PRIOR APPLICATION NUMBER: 09/259,214
 13 <151> PRIOR FILING DATE: 1999-03-01
 14 <160> NUMBER OF SEQ ID NOS: 4
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1323
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Escherichia coli
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (1)...(1320)
 24 <221> NAME/KEY: misc_feature
 25 <222> LOCATION: (1)...(1323)
 26 <223> OTHER INFORMATION: n = A,T,C or G
 27 <400> SEQUENCE: 1

ENTERED

28	atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg tta acc	48
29	Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr	
30	1 5 10 15	
31	ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt	96
32	Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
33	20 25 30	
34	gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg	144
35	Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
36	35 40 45	
37	caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta	192
38	Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
39	50 55 60	
W--> 40	aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc	240
41	Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
42	65 70 75 80	
43	gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa	288
44	Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	

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45		85	90	95	
46	aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac				336
47	Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp				
48		100	105	110	
49	gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct				384
50	Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro				
51		115	120	125	
52	gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat				432
53	Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp				
54		130	135	140	
55	ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg				480
56	Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala				
57		145	150	155	160
58	aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac				528
59	Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp				
60		165	170	175	
61	ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt				576
62	Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu				
63		180	185	190	
64	aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa				624
65	Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu				
66		195	200	205	
67	agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc				672
68	Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala				
69		210	215	220	
70	gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg				720
71	Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr				
72		225	230	235	240
73	gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg				768
74	Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp				
75		245	250	255	
76	gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat				816
77	Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His				
78		260	265	270	
79	aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc				864
80	Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser				
81		275	280	285	
82	cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat				912
83	Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His				
84		290	295	300	
85	cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg				960
86	Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu				
87		305	310	315	320
88	ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg				1008
89	Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu				
90		325	330	335	
91	gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt				1056
92	Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly				
93		340	345	350	

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```

94      ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag      1104
95      Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
96      355                                360                                365
97      tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat      1152
98      Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
99      370                                375                                380
100     aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc      1200
101     Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
102     385                                390                                395                                400
103     ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca      1248
104     Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
105     405                                410                                415
106     ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg      1296
107     Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
108     420                                425                                430
109     aga tct cat cac cat cac cat cac taa      1323
110     Arg Ser His His His His His His
111     435                                440
113 <210> SEQ ID NO: 2
114 <211> LENGTH: 440
115 <212> TYPE: PRT
116 <213> ORGANISM: Escherichia coli
117 <400> SEQUENCE: 2
118     Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
119     1      5      10      15
120     Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
121     20      25      30
122     Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
123     35      40      45
124     Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
125     50      55      60
126     Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
127     65      70      75      80
128     Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
129     85      90      95
130     Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
131     100     105     110
132     Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
133     115     120     125
134     Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
135     130     135     140
136     Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
137     145     150     155     160
138     Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
139     165     170     175
140     Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
141     180     185     190
142     Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
143     195     200     205

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144 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
145      210      215      220
146 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
147      225      230      235      240
148 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
149      245      250      255
150 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
151      260      265      270
152 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
153      275      280      285
154 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
155      290      295      300
156 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
157      305      310      315      320
158 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
159      325      330      335
160 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
161      340      345      350
162 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
163      355      360      365
164 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
165      370      375      380
166 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
167      385      390      395      400
168 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
169      405      410      415
170 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
171      420      425      430
172 Arg Ser His His His His His His
173      435      440
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 49
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Oligonucleotide
181 <400> SEQUENCE: 3
182 gtttctgaat tcaaggagga atttaaataa aagcgatctt aatcccatt
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 33
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Oligonucleotide
190 <400> SEQUENCE: 4
191 gtttctggat ccttacaac tgcacgccgg tat

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/034,985

DATE: 02/28/2002

TIME: 10:23:12

Input Set : N:\Crf3\RULE60\10034985.raw.txt

Output Set: N:\CRF3\02282002\J034985.raw

L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1